Amendments to Claims

Claim 1 (Original). A method for the production of a carotenoid compound comprising:

(a) providing a transformed C1 metabolizing host cell comprising:
  (i) suitable levels of isopentenyl pyrophosphate; and
  (ii) at least one isolated nucleic acid molecule encoding an enzyme in the carotenoid biosynthetic pathway under the control of suitable regulatory sequences;

(b) contacting the host cell of step (a) under suitable growth conditions with an effective amount of a C1 carbon substrate whereby an carotenoid compound is produced.

Claim 2 (Original). A method according to Claim 1 wherein the C1 carbon substrate is selected from the group consisting of methane, methanol, formaldehyde, formic acid, methylated amines, methylated thiols, and carbon dioxide.

Claim 3 (Original). A method according to Claim 1 wherein the C1 metabolizing host cell is a methylotroph selected from the group consisting of *Methylomonas, Methylobacter, Mehtylococcus, Methylosinus, Methylocyctis, Methylomicrobium, Methanomonas, Methylophilus, Methylobacillus, Methylobacterium, Hyphomicrobium, Xanthobacter, Bacillus, Paracoccus, Nocardia, Arthrobacter, Rhodopseudomonas, Pseudomonas, Candida, Hansenula, Pichia, Torulopsis,* and *Rhodotorula*

Claim 4 (Original). A method according to Claim 3 wherein C1 metabolizing host is a methanotroph.

Claim 5 (Canceled).

Claim 6 (Original). A method according to Claim 2 wherein the C1 carbon substrate is selected from the group consisting of methane and methanol and the C1 metabolizing host cell is a methanotroph selected from the group consisting of *Methylomonas, Methylobacter, Mehtylococcus, Methylosinus, Methylocyctis, Methylomicrobium,* and *Methanomonas.*

Claim 7 (Original). A method according to Claim 6 wherein the methanotroph is a high growth methanotrophic strain which comprises a functional Embden-Meyerhof carbon pathway, said pathway comprising a gene encoding a pyrophosphate dependent phosphofructokinase enzyme.

Claim 8 (Currently Amended). A method according to Claim 7 wherein the gene encoding a pyrophosphate dependent phosphofructokinase enzyme ~~is selected from the group consisting of:~~has the amino acid sequence as set forth in

~~(a) an isolated nucleic acid molecule encoding the amino acid sequence as set forth in~~ SEQ ID NO:2.~~;~~

~~(b) an isolated nucleic acid molecule that hybridizes with (a) under the following hybridization conditions: 0.1X SSC, 0.1% SDS, 65°C and washed with 2X SSC, 0.1% SDS followed by 0.1X SSC, 0.1% SDS;~~

~~(c) an isolated nucleic acid molecule comprising a first nucleotide sequence encoding a polypeptide of at least 437 amino acids that has at least 63% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO:2; and~~

~~(d) an isolated nucleic acid molecule that is complementary to (a), (b) or (c).~~

Claim 9 (Canceled).

Claim 10(Original). A method according to Claim 7 wherein the high growth methanotrophic bacterial strain optionally contains a functional Entner-Douderoff carbon pathway.

Claim 11 (Canceled).

Claim 12 (Currently Amended). A method according to Claim 79 wherein the high growth methanotrophic bacterial strain is methylomonas 16a having the ATCC designation ATCC PTA 2402.

Claim 13 (Original). A method according to Claim 1 wherein the isolated nucleic acid molecule encodes a carotenoid biosynthetic enzyme selected from the group consisting of geranylgeranyl pyrophosphate (GGPP) synthase, phytoene synthase, phytoene desaturase, lycopene cyclase, β-carotene hydroxylase, zeaxanthin glucosyl transferase, β-carotene ketolase, β-carotene C-4 oxygenase, β-carotene desaturase, spheroidene monooxygenase, carotene hydratase, carotenoid 3,4-desaturase, 1-OH-carotenoid methylase, farnesyl diphosphate synthetase, and diapophytoene dehydrogenase.

Claim 14 (Canceled).

Claim 15 (Original). A method according to Claim 13 wherein the geranylgeranyl pyrophosphate (GGPP) synthase as the amino acid sequence as set forth in SEQ ID NO:.26.

Claim 16 (Canceled).

Claim 17 (Original). A method according to Claim 13 wherein the phytoene synthase as the amino acid sequence as set forth in SEQ ID NO:34.

Claim 18 (Canceled).

Claim 19 (Original). A method according to Claim 13 wherein the phytoene desaturase as the amino acid sequence as set forth in SEQ ID NO:32.

Claim 20 (Canceled).

Claim 21 (Original). A method according to Claim 13 wherein the lycopene cyclase as the amino acid sequence as set forth in SEQ ID NO:30.

Claim 22 (Canceled).

Claim 23 (Original). A method according to Claim 13 wherein β-carotene hydroxylase as the amino acid sequence as set forth in SEQ ID NO:36.

Claim 24 (Canceled).

Claim 25 (Original). A method according to Claim 13 wherein zeaxanthin glucosyl transferase as the amino acid sequence as set forth in SEQ ID NO:28.

Claim 26 (Canceled).

Claim 27 (Original). A method according to Claim 13 wherein the isolated nucleic acid molecule encoding a carotenoid biosynthetic enzyme encodes a β-carotene ketolase having the amino acid sequence as set for the in SEQ ID NO:38.

Claim 28-34 (Canceled).

Claim 35 (Original). A method according to Claim 13 wherein the isolated nucleic acid molecule encoding a carotenoid biosynthetic enzyme encodes a farnesyl diphosphate synthetase having the amino acid sequence as set forth in SEQ ID NO:20.

Claim 36 (Canceled).

Claim 37 (Original). A method according to Claim 13 wherein the isolated nucleic acid molecule encoding a carotenoid biosynthetic enzyme encodes a diapophytoene dehydrogenase enzyme having the amino acid sequence selected from the group consisting of SEQ ID NO:22 and SEQ ID NO:24.

Claim 38 (Original). A method according to Claim 1 wherein said methanotrophic bacteria is *methylomonas* 16a ATCC PTA 2402.

Claim 39 (Currently Amended). A method according to Claim 1 wherein the suitable levels of isopentenyl pyrophosphate are provided by the expression of heterologous upper pathway isoprenoid pathway genes.

Claim 40 (Original). A method according to Claim 39 wherein said upper pathway isoprenoid genes are selected from the group consisting of D-1-deoxyxylulose-5-phosphate synthase (*Dxs*), D-1-deoxyxylulose-5-phosphate reductoisomerase (*Dxr*), 2C-methyl-d-erythritol cytidylyltransferase (*IspD*), 4-diphosphocytidyl-2-C-methylerythritol kinase (*IspE*), 2C-methyl-d-erythritol 2,4-cyclodiphosphate synthase (*IspF*), CTP synthase (*PyrG*), lytB, and GcpE.

Claim 41-47 (Canceled).

Claim 48 (Currently Amended). A method according to Claim 1 wherein the carotenoid compound is selected ~~form~~ from the group consisting of aAntheraxanthin, adonixanthin, aAstaxanthin, cCanthaxanthin, capsorubrin, β–cryptoxanthin alpha-carotene, beta-carotene, epsilon-carotene, echinenone, gamma-carotene, zeta-carotene, alpha-cryptoxanthin, diatoxanthin, 7,8-didehydroastaxanthin, fucoxanthin, fucoxanthinol, isorenieratene, lactucaxanthin, lutein, lycopene, neoxanthin, neurosporene, hydroxyneurosporene, peridinin, phytoene, rhodopin, rhodopin glucoside, siphonaxanthin,

spheroidene, spheroidenone, spirilloxanthin, uriolide, uriolide acetate, violaxanthin, zeaxanthin-β-diglucoside, and zeaxanthin.

Claim 49 (Original). A method for the over-production of carotenoid production in a transformed C1 metabolizing host comprising:

(a) providing a transformed C1 metabolizing host cell comprising:

(i) suitable levels of isopentenyl pyrophosphate; and

(ii) at least one isolated nucleic acid molecule encoding an enzyme in the carotenoid biosynthetic pathway under the control of suitable regulatory sequences; and

(iii) either:

1) multiple copies of at least one gene encoding an enzyme selected from the group consisting of D-1-deoxyxylulose-5-phosphate synthase (*Dxs*), D-1-deoxyxylulose-5-phosphate reductoisomerase (*Dxr*), 2C-methyl-d-erythritol cytidylyltransferase (*IspD*), 4-diphosphocytidyl-2-C-methylerythritol kinase (*IspE*), 2C-methyl-d-erythritol 2,4-cyclodiphosphate synthase (*IspF*), CTP synthase (*PyrG*) lytB and gcpE; or

2) at least one gene encoding an enzyme selected from the group consisting of D-1-deoxyxylulose-5-phosphate synthase (*Dxs*), D-1-deoxyxylulose-5-phosphate reductoisomerase (*Dxr*), 2C-methyl-d-erythritol cytidylyltransferase (*IspD*), 4-diphosphocytidyl-2-C-methylerythritol kinase (*IspE*), 2C-methyl-d-erythritol 2,4-cyclodiphosphate synthase (*IspF*), CTP synthase (*PyrG*), lytB and gcpE operably linked to a strong promoter.

(b) contacting the host cell of step (a) under suitable growth conditions with an effective amount of a C1 carbon substrate whereby a carotenoid compound is over-produced.

Claim 50 (Original). A method according to Claim 49 wherein the at least one gene encoding an enzyme of either part (a)(iii)(1) or (a)(iii)(2) encodes an enzyme selected from the group consisting of SEQ ID NO:6, 8, 10, 12, 14, 16, and 18.